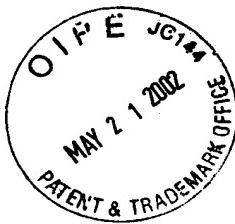


#3



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## SEQUENCE LISTING

*Jub*  
PO

<110> Abbott Laboratories  
Mukerji, Pradip  
Huang, Yung-Sheng  
Das, Tapas  
Thurmond, Jennifer M.  
Pereira, Suzette L.  
Leonard, Amanda E.

<120> DESATURASE GENES AND USES THEREOF

<130> 6763.US.P1

<140> 10/054,534  
<141> 2002-01-22

<150> US 09/769,863  
<151> 2001-01-25

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<223> y = t/u or c at position 9

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<223> b = g or c or t/u at position 12

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<223> r = g or a at position 18

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<223> b = g or c or t/u at position 24

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<221> misc_feature
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<222> (41)...(41)
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gggcytccg cyaactggtg gaagcaycag cayaacgtbc aycay 45
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<223> v = a or g or c at position 7

<221> misc_feature
<222> (13)...(13)
<223> r = g or a at position 13

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<222> (19)...(19)
<223> r = g or a at position 19

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<223> r = g or a at position 34

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<223> d = a or g or t/u at position 43

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<223> r = g or a at position 6

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<223> r = g or a at position 12

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<222> (15)...(15)
<223> y = t/u or c at position 15

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<223> r = g or a at position 18

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<223> r = g or a at position 21

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<221> misc_feature
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<223> r = g or a at position 27

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<221> misc_feature
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<223> r = g or a at position 13

<221> misc_feature

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<222> (16)...(16)
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<221> misc_feature
<222> (22)...(22)
<223> r = g or a at position 22

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<211> 30
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<223> y = t/u or c at position 18

<221> misc_feature
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<221> misc_feature
<222> (24)...(24)
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<221> misc_feature
<222> (27)...(27)
<223> n = a or g or c or t/u, unknown, or other at
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<221> misc_feature
<222> (30)...(30)
<223> y = t/u or c at position 30

<400> 6
ctactactac tacaycayac ntayacnaay

<210> 7
<211> 29
<212> DNA
<213> Artificial Sequence

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24

30

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<211> 30		
<212> DNA		
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<223> Primer RO899		
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<211> 30		
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<211> 31		
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<223> Primer RO898		
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cccagtcacg acgttgtaaa acgacggcca g		31
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<223> Primer RO951		
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tcaacagaat tcatggtcca ggggcaaaag gccgagaaga tctcg		45
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<223> Primer RO960		

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 <212> DNA  
 <213> Saprolegnia diclina

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 caccggggcg gcgtcgcat gttcacgcag gccggcgaag acgcgaccga tgcgttcgct 180  
 gtcttccacc cgagctcgcc gctcaagtc ctcgagcagt actacgtcgg cgacgtcgac 240  
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 gcccatttgc tccactttga ctcgacggcc atgtacatgg tcgcccgtt catccttgc 480  
 ctctttacc agcagtgcgg ctggctcgcc catgacttc tgaccacca agtgttttag 540  
 aaccacttgt ttggcgacct cgtccgcgtc atggcggca acctctggca gggcttctcg 600  
 gtgcagtgtt ggaagaacaa gcacaacacg caccatgcga tccccaacct ccacgcgacg 660  
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 aagcccgatt tttggaaagct gcaagtgcgc tcgacgcgc acgtgacgtc gtcgtctgg 1140  
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 <213> Saprolegnia diclina

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 Tyr Asp Ile Ser Ala Phe Glu Asp His Pro Gly Gly Val Val Met Phe  
 35 40 45  
 Thr Gln Ala Gly Glu Asp Ala Thr Asp Ala Phe Ala Val Phe His Pro  
 50 55 60  
 Ser Ser Ala Leu Lys Leu Leu Glu Gln Tyr Tyr Val Gly Asp Val Asp  
 65 70 75 80  
 Gln Ser Thr Ala Ala Val Asp Thr Ser Ile Ser Asp Glu Val Lys Lys  
 85 90 95  
 Ser Gln Ser Asp Phe Ile Ala Ser Tyr Arg Lys Leu Arg Leu Glu Val  
 100 105 110  
 Lys Arg Leu Gly Leu Tyr Asp Ser Ser Lys Leu Tyr Tyr Leu Tyr Lys  
 115 120 125  
 Cys Ala Ser Thr Leu Ser Ile Ala Leu Val Ser Ala Ala Ile Cys Leu

130	135	140													
His	Phe	Asp	Ser	Thr	Ala	Met	Tyr	Met	Val	Ala	Ala	Val	Ile	Leu	Gly
145						150				155					160
Leu	Phe	Tyr	Gln	Gln	Cys	Gly	Trp	Leu	Ala	His	Asp	Phe	Leu	His	His
						165			170						175
Gln	Val	Phe	Glu	Asn	His	Leu	Phe	Gly	Asp	Leu	Val	Gly	Val	Met	Val
						180			185						190
Gly	Asn	Leu	Trp	Gln	Gly	Phe	Ser	Val	Gln	Trp	Trp	Lys	Asn	Lys	His
						195			200						205
Asn	Thr	His	His	Ala	Ile	Pro	Asn	Leu	His	Ala	Thr	Pro	Glu	Ile	Ala
						210			215						220
Phe	His	Gly	Asp	Pro	Asp	Ile	Asp	Thr	Met	Pro	Ile	Leu	Ala	Trp	Ser
						225			230			235			240
Leu	Lys	Met	Ala	Gln	His	Ala	Val	Asp	Ser	Pro	Val	Gly	Leu	Phe	Phe
						245			250						255
Met	Arg	Tyr	Gln	Ala	Tyr	Leu	Tyr	Phe	Pro	Ile	Leu	Leu	Phe	Ala	Arg
						260			265						270
Ile	Ser	Trp	Val	Ile	Gln	Ser	Ala	Met	Tyr	Ala	Phe	Tyr	Asn	Val	Gly
						275			280						285
Pro	Gly	Gly	Thr	Phe	Asp	Lys	Val	Gln	Tyr	Pro	Leu	Leu	Glu	Arg	Ala
						290			295			300			
Gly	Leu	Leu	Leu	Tyr	Tyr	Gly	Trp	Asn	Leu	Gly	Leu	Val	Tyr	Ala	Ala
						305			310			315			320
Asn	Met	Ser	Leu	Leu	Gln	Ala	Ala	Ala	Phe	Leu	Phe	Val	Ser	Gln	Ala
						325			330						335
Ser	Cys	Gly	Leu	Phe	Leu	Ala	Met	Val	Phe	Ser	Val	Gly	His	Asn	Gly
						340			345						350
Met	Glu	Val	Phe	Asp	Lys	Asp	Ser	Lys	Pro	Asp	Phe	Trp	Lys	Leu	Gln
						355			360						365
Val	Leu	Ser	Thr	Arg	Asn	Val	Thr	Ser	Ser	Leu	Trp	Ile	Asp	Trp	Phe
						370			375			380			
Met	Gly	Gly	Leu	Asn	Tyr	Gln	Ile	Asp	His	His	Leu	Phe	Pro	Met	Val
						385			390			395			400
Pro	Arg	His	Asn	Leu	Pro	Ala	Leu	Asn	Val	Leu	Val	Lys	Ser	Leu	Cys
						405			410						415
Lys	Gln	Tyr	Asp	Ile	Pro	Tyr	His	Glu	Thr	Gly	Phe	Ile	Ala	Gly	Met
						420			425						430
Ala	Glu	Val	Val	Val	His	Leu	Glu	Arg	Ile	Ser	Ile	Glu	Phe	Phe	Lys
						435			440						445
Glu	Phe	Pro	Ala	Met											
						450									

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<223> Primer R0851

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<210> 16  
<211> 28  
<212> DNA

<213> Artificial Sequence

<220>

<223> Primer R0941

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gctgaacggg tggtacgagt cgaacgtg

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<210> 17

<211> 42

<212> DNA

<213> Artificial Sequence

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<223> Primer R0953

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42

<210> 18

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer R0956

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46

<210> 19

<211> 1413

<212> DNA

<213> Saprolegnia diclina

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 atcatttatcc gcggcaaggct ctacgacgtg accgagtggg ccaacaagca ccccgccggc 180  
 cgcgagatgg tgctgctgca cgccggctgc gaggccaccc acacgttcga ctgttaccac 240  
 ccgttcagcg acaaggccga gtcgatcttgc aacaagtatg agatggcac gttcacgggc 300  
 ccgtccgatgt ttccgaccc caagccggac acgggcttct acaaggatgt cgcgaagcgc 360  
 gttggcgatgt acttcaagaa gaacaacctc catccgcagg acggcttccc gggctctgg 420  
 cgcgtatgg tgcgttttc ggtcgccgg ctgcgccttg acggcatgca ttttcgact 480  
 atctttgcgc tgcagctcgc ggccgcggcg ctctttggcg tctgccaggc gctgccgtg 540  
 ctccacgtca tgcacgactc gtcgcacgcg tcgtacacca acatccgtt cttccattac 600  
 gtcgtccggcc gcttgcctt ggactgggtt gccggcggtt cgtatggatgtc atggctcaac 660  
 cagcacgtcg tgggcccacca catctacacg aacgtcgccg gctccggaccc ggtatcttcg 720  
 gtcaacatgg acggcgacat ccgcgcgcgcgtc gtgaaccggcc aggtgttcca gcccacgtac 780  
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 ggcgcgtca actaccaggatgtt cgtgcaccac ttgttccca ggcgtcgca gtaccactac 1260

ccggcgatcg cgcccatcat cgtcgacgac tgcaaggagt acaaactaa gtacgccatc 1320  
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 <213> Saprolegnia diclina

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 20 25 30  
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 35 40 45  
 Asp Val Thr Glu Trp Ala Asn Lys His Pro Gly Gly Arg Glu Met Val  
 50 55 60  
 Leu Leu His Ala Gly Arg Glu Ala Thr Asp Thr Phe Asp Ser Tyr His  
 65 70 75 80  
 Pro Phe Ser Asp Lys Ala Glu Ser Ile Leu Asn Lys Tyr Glu Ile Gly  
 85 90 95  
 Thr Phe Thr Gly Pro Ser Glu Phe Pro Thr Phe Lys Pro Asp Thr Gly  
 100 105 110  
 Phe Tyr Lys Glu Cys Arg Lys Arg Val Gly Glu Tyr Phe Lys Lys Asn  
 115 120 125  
 Asn Leu His Pro Gln Asp Gly Phe Pro Gly Leu Trp Arg Met Met Val  
 130 135 140  
 Val Phe Ala Val Ala Gly Leu Ala Leu Tyr Gly Met His Phe Ser Thr  
 145 150 155 160  
 Ile Phe Ala Leu Gln Leu Ala Ala Ala Leu Phe Gly Val Cys Gln  
 165 170 175  
 Ala Leu Pro Leu Leu His Val Met His Asp Ser Ser His Ala Ser Tyr  
 180 185 190  
 Thr Asn Met Pro Phe Phe His Tyr Val Val Gly Arg Phe Ala Met Asp  
 195 200 205  
 Trp Phe Ala Gly Gly Ser Met Val Ser Trp Leu Asn Gln His Val Val  
 210 215 220  
 Gly His His Ile Tyr Thr Asn Val Ala Gly Ser Asp Pro Asp Leu Pro  
 225 230 235 240  
 Val Asn Met Asp Gly Asp Ile Arg Arg Ile Val Asn Arg Gln Val Phe  
 245 250 255  
 Gln Pro Met Tyr Ala Phe Gln His Ile Tyr Leu Pro Pro Leu Tyr Gly  
 260 265 270  
 Val Leu Gly Leu Lys Phe Arg Ile Gln Asp Phe Thr Asp Thr Phe Gly  
 275 280 285  
 Ser His Thr Asn Gly Pro Ile Arg Val Asn Pro His Ala Leu Ser Thr  
 290 295 300  
 Trp Met Ala Met Ile Ser Ser Lys Ser Phe Trp Ala Phe Tyr Arg Val  
 305 310 315 320  
 Tyr Leu Pro Leu Ala Val Leu Gln Met Pro Ile Lys Thr Tyr Leu Ala  
 325 330 335  
 Ile Phe Phe Leu Ala Glu Phe Val Thr Gly Trp Tyr Leu Ala Phe Asn  
 340 345 350  
 Phe Gln Val Ser His Val Ser Thr Glu Cys Gly Tyr Pro Cys Gly Asp  
 355 360 365  
 Glu Ala Lys Met Ala Leu Gln Asp Glu Trp Ala Val Ser Gln Val Lys

370	375	380
Thr Ser Val Asp Tyr Ala His Gly Ser Trp Met		Thr Thr Phe Leu Ala
385	390	395
Gly Ala Leu Asn Tyr Gln Val Val His His		Leu Phe Pro Ser Val Ser
405		410
Gln Tyr His Tyr Pro Ala Ile Ala Pro Ile Ile Val Asp Val Cys Lys		415
420	425	430
Glu Tyr Asn Ile Lys Tyr Ala Ile Leu Pro Asp Phe Thr Ala Ala Phe		435
435	440	445
Val Ala His Leu Lys His Leu Arg Asn Met Gly Gln Gln Gly Ile Ala		450
450	455	460
Ala Thr Ile His Met Gly		465
	470	

&lt;210&gt; 21

&lt;211&gt; 914

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 21

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 atatatttac taattgtatg gctgggacca aaatacatga ggaataaaaca gccattctct 180  
 tgccggggga ttttagtgggt gtataaacctt ggactcacac tgctgtctct gtatatgttc 240  
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 accgcaggag aatcagatata gaagattatac cgtgtcctct ggtggacta cttctccaaa 360  
 ctcatagaat ttatggacac tttcttcttc atcctgcgca agaacaacca ccagatcacg 420  
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 cgaaggaaag accacacgtt gggaccaccag aatgggtccg tggctgtgt gaatggacac 840  
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 agtcaaagaa ttga 914

&lt;210&gt; 22

&lt;211&gt; 957

&lt;212&gt; DNA

&lt;213&gt; Mortierella alpina

&lt;400&gt; 22

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 gcccagccgc agaagtacat cccccacgatt gtccatcaca cgcgctgggtt cctggtcgcg 180  
 gtggagtcgc cttggcccg tgagctgccg ttgatgaacc cggtccacgt gctgttgatc 240  
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 aagatcatgg agtttgcga caccatgatc atggctctca agaagaacaa ccggccagatc 540  
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 atgtacggct actacttctt gtcggccttgg ggttcaagc aggtgtcggtt catcaagttc 720  
 tacatcacgc gctcgacat gacacagttc tgcgtatgtt cggccagtc ttccctggac 780

atgtacgcca tgaaggctt tggccgcccc ggataccct tcttcatcac ggctctgctt 840  
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<220>  
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<220>  
 <223> Primer R0937

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<220>  
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<400> 25  
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<210> 26  
 <211> 39  
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<220>  
 <223> Primer R0949

<400> 26  
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 <213> Artificial Sequence

<220>  
 <223> Primer R0950

<400> 27

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 atcacgcgag actacgtcaa gctgcgcgag gagatggtgcc cgagggccct cttcaagccc 360  
 gcgccctcc acattgtcta caggtttcgag gagatcgccg ccctgttcgc ggcctcggttc 420  
 tacctgtttt cgatgcgcgg aaacgtgttc gecacgctcg cggccatcgc agtcggggc 480  
 atcgcgcagg gccgctcggt ctggctcatg cacgagtgcg gacacttctc gatgaccggg 540  
 tacatcccgcc ttgacgtgcg cctgcaggag ctgggtgtacg gctgtgggtg ctcgatgtcg 600  
 gcgagcttgtt ggcgcgttca gcacaacaag caccacgcga ccccgagaa actcaagcac 660  
 gacgtcgacc tcgacaccct gccgctcggtt gcgttcaacg agaagatcgc cgccaaagggtg 720  
 cgcccccgcgt cggtccaggc caagtggcgc tccggcgcagg cgtacatttt tgccgcccgg 780  
 tcctgttcc ttgggtgtct cttdtgcacc ctgggtgtacg acccgcccca catgcccgcgc 840  
 acgagccact ttgctgagat ggccgcgtc gccgtgcgcg tcgtgggtcg ggcggcgcgc 900  
 atgcactcgt tcgggtacag cgggagcgac tcgttgcggc tctacatggc cacccttggc 960  
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 aacgactcgt ggttcatcac ctgggtgatg tcgtacactca actttcagat cgagcaccac 1140  
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 ttcgagaagc acggcatggc ttacgacgag cggccgttacc ttaccgcgt tggcgacacg 1260  
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<210> 29  
<211> 439  
<212> PRT  
<213> Thraustochytrium aureum

<400> 29

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	Gly	Ala	Gly	Thr	Arg	Lys	Thr	Ile	Leu	Ile	Glu	Gly	Glu	Val	Tyr	
				20					25						30	
	Sp	Val	Thr	Asn	Phe	Arg	His	Pro	Gly	Gly	Ser	Ile	Ile	Lys	Phe	Leu
				35					40						45	
	Tr	Thr	Asp	Gly	Thr	Glu	Ala	Val	Asp	Ala	Thr	Asn	Ala	Phe	Arg	Glu
				50					55						60	
	He	His	Cys	Arg	Ser	Gly	Lys	Ala	Glu	Lys	Tyr	Leu	Lys	Ser	Leu	Pro
				5					70						75	80
	Ys	Leu	Gly	Ala	Pro	Ser	Lys	Met	Lys	Phe	Asp	Ala	Lys	Glu	Gln	Ala
				85					90						95	
	Rg	Arg	Asp	Ala	Ile	Thr	Arg	Asp	Tyr	Val	Lys	Leu	Arg	Glu	Glu	Met
				100					105						110	
	A	Ala	Glu	Gly	Leu	Phe	Lys	Pro	Ala	Pro	Leu	His	Ile	Val	Tyr	Arg
				115					120						125	
	E	Ala	Glu	Ile	Ala	Ala	Leu	Phe	Ala	Ala	Ser	Phe	Tyr	Leu	Phe	Ser
				130					135						140	
	M	et	Arg	Gly	Asn	Val	Phe	Ala	Thr	Leu	Ala	Ala	Ile	Ala	Val	Gly

145	150	155	160
Ile Ala Gln Gly Arg Cys Gly Trp Leu Met His Glu Cys Gly His Phe			
165	170	175	
Ser Met Thr Gly Tyr Ile Pro Leu Asp Val Arg Leu Gln Glu Leu Val			
180	185	190	
Tyr Gly Val Gly Cys Ser Met Ser Ala Ser Trp Trp Arg Val Gln His			
195	200	205	
Asn Lys His His Ala Thr Pro Gln Lys Leu Lys His Asp Val Asp Leu			
210	215	220	
Asp Thr Leu Pro Leu Val Ala Phe Asn Glu Lys Ile Ala Ala Lys Val			
225	230	235	240
Arg Pro Gly Ser Phe Gln Ala Lys Trp Leu Ser Ala Gln Ala Tyr Ile			
245	250	255	
Phe Ala Pro Val Ser Cys Phe Leu Val Gly Leu Phe Trp Thr Leu Phe			
260	265	270	
Leu His Pro Arg His Met Pro Arg Thr Ser His Phe Ala Glu Met Ala			
275	280	285	
Ala Val Ala Val Arg Val Val Gly Trp Ala Ala Leu Met His Ser Phe			
290	295	300	
Gly Tyr Ser Gly Ser Asp Ser Phe Gly Leu Tyr Met Ala Thr Phe Gly			
305	310	315	320
Phe Gly Cys Thr Tyr Ile Phe Thr Asn Phe Ala Val Ser His Thr His			
325	330	335	
Leu Asp Val Thr Glu Pro Asp Glu Phe Leu His Trp Val Glu Tyr Ala			
340	345	350	
Ala Leu His Thr Thr Asn Val Ser Asn Asp Ser Trp Phe Ile Thr Trp			
355	360	365	
Trp Met Ser Tyr Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Ser			
370	375	380	
Leu Pro Gln Leu Asn Ala Pro Arg Val Ala Pro Arg Val Arg Ala Leu			
385	390	395	400
Phe Glu Lys His Gly Met Ala Tyr Asp Glu Arg Pro Tyr Leu Thr Ala			
405	410	415	
Leu Gly Asp Thr Phe Ala Asn Leu His Ala Val Gly Gln Asn Ala Gly			
420	425	430	
Gln Ala Ala Ala Lys Ala Ala			
435			

&lt;210&gt; 30

&lt;211&gt; 1338

&lt;212&gt; DNA

&lt;213&gt; Thraustochytrium aureum

&lt;400&gt; 30

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agcccaagtg	agcagcgtaa	ggtgttgctc	attgacgggc	agctgtacga	tgcaccaac	120
ttcaggcattc	ctgggtggctc	catcatcaaa	tatttgtgca	ccgatggcaa	ggaggttagtt	180
gatgcaaccg	aagcgtaaa	ggagttccac	tgcagatcc	cgaaggcggt	caagtacotc	240
aactccctgc	caaagatcga	cggcccaatc	aagtacaat	acgacgaaa	ggagcgaggct	300
cgccatgaca	aactcacgag	ggagtatgtt	gctctccgct	aacagtcgt	caaggagggta	360
tactttgacc	ccagccccgt	ccacatttac	tacagatgcg	ccgagttggc	agccatgttc	420
gctctctcg	tctacctttt	ctccttcaag	ggtAACgtca	tggccactat	tgctgcccattc	480
gtgattgggg	ggtgcgtgca	gggtcggtgt	gggtggctca	tgcataaagc	tggccactac	540
aagcatgaccg	gaaacatccc	tgttgacttg	cgccttcaag	agttttgtt	cggaattggg	600
tgtggcatga	gcggggcttg	gtggagaagc	cagcacaaca	agcaccacgc	caccccccacaa	660
aagctcaagc	atgacgttga	tttggacact	cttccttcttg	tcgcctggaa	cgagaaaatt	720

gcccgtcgcg	tcaagccagg	tagcttccag	gcaaagtggc	ttcatctcca	gggatacatc	780
tttgccccag	tctcctgcct	tctcggttgg	ctcttctgga	ctttgtactt	gcatcctcgc	840
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ctcaaggata	cttcggccaa	cctacacgaa	gtgggcgtca	acgctggcca	agctgccaag	1320
agcgagtaag	atctcgag					1338

&lt;210&gt; 31

&lt;211&gt; 439

&lt;212&gt; PRT

&lt;213&gt; Thraustochytrium aureum

&lt;400&gt; 31

Met	Gly	Arg	Gly	Ala	Gln	Gly	Glu	Pro	Arg	Gln	Ala	Thr	Glu	Leu	Lys
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Ser	Ser	Pro	Ser	Glu	Gln	Arg	Lys	Val	Leu	Leu	Ile	Asp	Gly	Gln	Leu
				20				25				30			
Tyr	Asp	Ala	Thr	Asn	Phe	Arg	His	Pro	Gly	Gly	Ser	Ile	Ile	Lys	Tyr
				35				40				45			
Leu	Cys	Thr	Asp	Gly	Lys	Glu	Val	Val	Asp	Ala	Thr	Glu	Ala	Tyr	Lys
				50				55				60			
Glu	Phe	His	Cys	Arg	Ser	Ser	Lys	Ala	Val	Lys	Tyr	Leu	Asn	Ser	Leu
				65				70				75			80
Pro	Lys	Ile	Asp	Gly	Pro	Ile	Lys	Tyr	Lys	Tyr	Asp	Ala	Lys	Glu	Gln
				85				90				95			
Ala	Arg	His	Asp	Lys	Leu	Thr	Arg	Glu	Tyr	Val	Ala	Leu	Arg	Glu	Gln
				100				105				110			
Leu	Val	Lys	Glu	Gly	Tyr	Phe	Asp	Pro	Ser	Pro	Leu	His	Ile	Ile	Tyr
				115				120				125			
Arg	Cys	Ala	Glu	Leu	Ala	Ala	Met	Phe	Ala	Leu	Ser	Phe	Tyr	Leu	Phe
				130				135				140			
Ser	Phe	Lys	Gly	Asn	Val	Met	Ala	Thr	Ile	Ala	Ile	Val	Ile	Gly	
				145				150				155			160
Gly	Cys	Val	Gln	Gly	Arg	Cys	Gly	Trp	Leu	Met	His	Glu	Ala	Gly	His
				165				170				175			
Tyr	Ser	Met	Thr	Gly	Asn	Ile	Pro	Val	Asp	Leu	Arg	Leu	Gln	Glu	Phe
				180				185				190			
Leu	Tyr	Gly	Ile	Gly	Cys	Gly	Met	Ser	Gly	Ala	Trp	Trp	Arg	Ser	Gln
				195				200				205			
His	Asn	Lys	His	His	Ala	Thr	Pro	Gln	Lys	Leu	Lys	His	Asp	Val	Asp
				210				215				220			
Leu	Asp	Thr	Leu	Pro	Leu	Val	Ala	Trp	Asn	Glu	Lys	Ile	Ala	Arg	Arg
				225				230				235			240
Val	Lys	Pro	Gly	Ser	Phe	Gln	Ala	Lys	Trp	Leu	His	Leu	Gln	Gly	Tyr
				245				250				255			
Ile	Phe	Ala	Pro	Val	Ser	Cys	Leu	Leu	Val	Gly	Leu	Phe	Trp	Thr	Leu
				260				265				270			
Tyr	Leu	His	Pro	Arg	His	Met	Ile	Arg	Thr	Lys	Arg	Asn	Phe	Glu	Ile
				275				280				285			
Phe	Ser	Val	Ala	Leu	Arg	Tyr	Val	Cys	Trp	Phe	Ser	Leu	Leu	Leu	Ser
				290				295				300			
Met	Gly	Tyr	Thr	Val	Gly	Glu	Ser	Leu	Gly	Leu	Tyr	Val	Leu	Thr	Phe

305	310	315	320
Gly Leu Gly Cys Thr Tyr Ile Phe Thr His Phe Ala Val Ser His Thr			
325	330	335	
His Leu Pro Val Ser Glu Glu Asp Glu Tyr Leu His Trp Val Glu Tyr			
340	345	350	
Ala Ala Leu His Thr Thr Asn Val Ala Ile Asp Ser Tyr Val Val Thr			
355	360	365	
Trp Leu Met Ser Tyr Leu Asn Phe Gln Ile Glu His His Leu Phe Pro			
370	375	380	
Cys Cys Pro Gln Phe Arg His Pro Ala Ile Ser Ser Arg Val Lys Lys			
385	390	395	400
Leu Phe Glu Asp Asn Gly Leu Val Tyr Asp Ala Arg Ser Tyr Val Gln			
405	410	415	
Ala Leu Lys Asp Thr Phe Gly Asn Leu His Glu Val Gly Val Asn Ala			
420	425	430	
Gly Gln Ala Ala Lys Ser Glu			
435			

&lt;210&gt; 32

&lt;211&gt; 1381

&lt;212&gt; DNA

&lt;213&gt; Thraustochytrium aureum

&lt;400&gt; 32

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cggactatct	cagaaaacac	cctggtgca	gcgtqatcaa	gtacgggctt	qccaacacccg	180
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gccgggatgg	attgatggaa	ccttccttct	ggcatcgccg	ttacagatta	ttagagcttg	420
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t						1381

&lt;210&gt; 33

&lt;211&gt; 456

&lt;212&gt; PRT

&lt;213&gt; Thraustochytrium aureum

&lt;400&gt; 33

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     20                       25                       30  
 Asn Gly Val Glu Tyr Asp Val Thr Asp Tyr Leu Arg Lys His Pro Gly  
     35                       40                       45  
 Gly Ser Val Ile Lys Tyr Gly Leu Ala Asn Thr Gly Ala Asp Ala Thr  
     50                       55                       60  
 Ser Leu Phe Glu Ala Phe His Met Arg Ser Lys Lys Ala Gln Met Val  
     65                       70                       75                       80  
 Leu Lys Ser Leu Pro Lys Arg Ala Pro Val Leu Glu Ile Gln Pro Asn  
     85                       90                       95  
 Gln Leu Pro Glu Glu Gln Thr Lys Glu Ala Glu Met Leu Arg Asp Phe  
     100                       105                       110  
 Lys Lys Phe Glu Asp Glu Ile Arg Arg Asp Gly Leu Met Glu Pro Ser  
     115                       120                       125  
 Phe Trp His Arg Ala Tyr Arg Leu Ser Glu Leu Val Gly Met Phe Thr  
     130                       135                       140  
 Leu Gly Leu Tyr Leu Phe Ser Leu Asn Thr Pro Leu Ser Ile Ala Ala  
     145                       150                       155                       160  
 Gly Val Leu Val His Gly Leu Phe Gly Ala Phe Cys Gly Trp Cys Gln  
     165                       170                       175  
 His Glu Ala Gly His Gly Ser Phe Phe Tyr Ser Leu Trp Trp Gly Lys  
     180                       185                       190  
 Arg Val Gln Ala Met Leu Ile Gly Phe Gly Leu Gly Thr Ser Gly Asp  
     195                       200                       205  
 Met Trp Asn Met Met His Asn Lys His His Ala Ala Thr Gln Lys Val  
     210                       215                       220  
 His His Asp Leu Asp Ile Asp Thr Thr Pro Phe Val Ala Phe Phe Asn  
     225                       230                       235                       240  
 Thr Ala Phe Glu Lys Asn Arg Trp Lys Gly Phe Ser Lys Ala Trp Val  
     245                       250                       255  
 Arg Phe Gln Ala Phe Thr Phe Ile Pro Val Thr Ser Gly Met Ile Val  
     260                       265                       270  
 Met Leu Phe Trp Leu Phe Phe Leu His Pro Arg Arg Val Val Gln Lys  
     275                       280                       285  
 Lys Asn Phe Glu Glu Gly Phe Trp Met Leu Ser Ser His Ile Val Arg  
     290                       295                       300  
 Thr Tyr Leu Phe His Leu Val Thr Gly Trp Glu Ser Leu Ala Ala Cys  
     305                       310                       315                       320  
 Tyr Leu Val Gly Tyr Trp Ala Cys Met Trp Val Ser Gly Met Tyr Leu  
     325                       330                       335  
 Phe Gly His Phe Ser Leu Ser His Thr His Met Asp Ile Val Glu Ala  
     340                       345                       350  
 Asp Val His Lys Asn Trp Val Arg Tyr Ala Val Asp His Thr Val Asp  
     355                       360                       365  
 Ile Ser Pro Ser Asn Pro Leu Val Cys Trp Val Met Gly Tyr Leu Asn  
     370                       375                       380  
 Met Gln Thr Ile His His Leu Trp Pro Ala Met Pro Gln Tyr His Gln  
     385                       390                       395                       400  
 Val Glu Val Ser Arg Arg Phe Ala Ile Phe Ala Lys Lys His Gly Leu  
     405                       410                       415  
 Asn Tyr Arg Val Val Ser Tyr Phe Glu Ala Trp Arg Leu Met Leu Gln  
     420                       425                       430  
 Asn Leu Ala Asp Val Gly Ser His Tyr His Glu Asn Gly Val Lys Arg  
     435                       440                       445  
 Ala Pro Lys Lys Ala Lys Ala Gln  
     450                       455

<210> 34  
<211> 1329  
<212> DNA  
<213> Isochrysis galbana

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atcgatgctg	aaaaggagat	gatcatcaac	ggccgcgtgt	atgacgtgtc	gtcatttgc	180
aaggcgccacc	caggtggctc	ggtgatcaag	ttccagctgg	gcgcgcacgc	gagcgacgcg	240
tacaacaact	ttcacgtccg	ctccaagaag	gcccacaaga	tgctgtattc	gctcccggtcc	300
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gtgctgtggc	acctggcctt	tggccacact	gggctgtga	gctcgctccg	cctgtacgcc	960
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accaactgtc	ccgactcgcc	ctttgtcaac	tggggatgg	cctacccaa	cttccagata	1140
gaggaccaccc	tcttcccgtc	gatgccgcag	tacaaccacc	ccaagatcg	cccgccgggt	1200
cgccgcgtct	tcgagaagca	cggggctcgag	tatgacgtcc	ggccataacct	ggagtgtttt	1260
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acgcacttag						1329

<210> 35  
<211> 442  
<212> PRT  
<213> Isochrysis galbana

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<400> 35
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      20          25          30
Ala Ala Asp Val Thr Val Ser Ser Ile Asp Ala Glu Lys Glu Met Ile
      35          40          45
Ile Asn Gly Arg Val Tyr Asp Val Ser Ser Phe Val Lys Arg His Pro
      50          55          60
Gly Gly Ser Val Ile Lys Phe Gln Leu Gly Ala Asp Ala Ser Asp Ala
      65          70          75          80
Tyr Asn Asn Phe His Val Arg Ser Lys Lys Ala Asp Lys Met Leu Tyr
      85          90          95
Ser Leu Pro Ser Arg Pro Ala Glu Ala Gly Tyr Ala Gln Asp Asp Ile
      100         105         110
Ser Arg Asp Phe Glu Lys Leu Arg Leu Glu Leu Lys Glu Glu Gly Tyr
      115         120         125
Phe Glu Pro Asn Leu Val His Val Ser Tyr Arg Cys Val Glu Val Leu
      130         135         140
Ala Met Tyr Trp Ala Gly Val Gln Leu Ile Trp Ser Gly Tyr Trp Phe
      145         150         155          160
Leu Gly Ala Ile Val Ala Gly Ile Ala Gln Gly Arg Cys Gly Trp Leu

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Gln	His	Glu	Gly	Gly	His	Tyr	Ser	Leu	Thr	Gly	Asn	Ile	Lys	Ile	Asp
165									170					175	
180								185						190	
Arg	His	Leu	Gln	Met	Ala	Ile	Tyr	Gly	Leu	Gly	Cys	Gly	Met	Ser	Gly
195								200						205	
Cys	Tyr	Trp	Arg	Asn	Gln	His	Asn	Lys	His	His	Ala	Thr	Pro	Gln	Lys
210								215						220	
Leu	Gly	Thr	Asp	Pro	Asp	Leu	Gln	Thr	Met	Pro	Leu	Val	Ala	Phe	His
225								230				235		240	
Lys	Ile	Val	Gly	Ala	Lys	Ala	Arg	Gly	Lys	Gly	Lys	Ala	Trp	Leu	Ala
								245			250			255	
Trp	Gln	Ala	Pro	Leu	Phe	Phe	Gly	Gly	Ile	Ile	Cys	Ser	Leu	Val	Ser
								260		265				270	
Phe	Gly	Trp	Gln	Phe	Val	Leu	His	Pro	Asn	His	Ala	Leu	Arg	Val	His
275								280				285			
Asn	His	Leu	Glu	Leu	Ala	Tyr	Met	Gly	Leu	Arg	Tyr	Val	Leu	Trp	His
290								295				300			
Leu	Ala	Phe	Gly	His	Leu	Gly	Leu	Leu	Ser	Ser	Leu	Arg	Leu	Tyr	Ala
305								310			315			320	
Phe	Tyr	Val	Ala	Val	Gly	Gly	Thr	Tyr	Ile	Phe	Thr	Asn	Phe	Ala	Val
								325		330				335	
Ser	His	Thr	His	Lys	Asp	Val	Val	Pro	Pro	Thr	Lys	His	Ile	Ser	Trp
								340		345				350	
Ala	Leu	Tyr	Ser	Ala	Asn	His	Thr	Thr	Asn	Cys	Ser	Asp	Ser	Pro	Phe
								355		360				365	
Val	Asn	Trp	Trp	Met	Ala	Tyr	Leu	Asn	Phe	Gln	Ile	Glu	His	His	Leu
								370		375				380	
Phe	Pro	Ser	Met	Pro	Gln	Tyr	Asn	His	Pro	Lys	Ile	Ala	Pro	Arg	Val
385								390			395			400	
Arg	Ala	Leu	Phe	Glu	Lys	His	Gly	Val	Glu	Tyr	Asp	Val	Arg	Pro	Tyr
								405		410				415	
Leu	Glu	Cys	Phe	Arg	Val	Thr	Tyr	Val	Asn	Leu	Leu	Ala	Val	Gly	Asn
								420		425				430	
Pro	Glu	His	Ser	Tyr	His	Glu	His	Thr	His						
								435		440					

&lt;210&gt; 36

&lt;211&gt; 36

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Primer RO838

&lt;221&gt; misc\_feature

&lt;222&gt; (7)...(7)

&lt;223&gt; v = a or g or c at position 7

&lt;221&gt; misc\_feature

&lt;222&gt; (10)...(10)

&lt;223&gt; r = g or a at position 10

&lt;221&gt; misc\_feature

&lt;222&gt; (13)...(13)

&lt;223&gt; s = g or c at position 13

&lt;221&gt; misc\_feature

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<222> (16)...(16)
<223> r = g or a at position 16

<221> misc_feature
<222> (19)...(19)
<223> r = g or a at position 19

<221> misc_feature
<222> (22)...(22)
<223> y = t/u or c at position 22

<221> misc_feature
<222> (25)...(25)
<223> r = g or a at position 25

<221> misc_feature
<222> (31)...(31)
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23

35

35

<223> Consensus Peptide Sequence

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Asn Tyr Gln Ile Glu His His Leu Phe Pro Thr Met  
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